

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:58:24 ; Search time 21 Seconds
(without alignments)
114.514 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 4988

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	29	21.3	25	2	S07770	histone H2B.1, spe
2	28	20.6	11	2	S78765	ribosomal protein
3	27	19.9	16	2	PHI351	Ig heavy chain DJ
4	27	19.9	20	2	A41439	acid ribonuclease
5	27	19.9	25	1	ZJBPG4	gene J protein - p
6	26.5	19.5	20	2	A36016	granulocyte inhibi
7	26.5	19.5	22	2	PQ0143	polygalacturonase
8	26	19.1	13	2	S32551	Glutathione transf
9	26	19.1	15	4	I38336	hypothetical TEL/M
10	26	19.1	20	2	JP0055	ribosomal protein
11	26	19.1	22	2	H30608	Ig kappa chain V-I
12	26	19.1	22	2	D30609	Ig kappa chain V-I
13	26	19.1	24	2	S30609	Ig kappa chain V-I
14	26	19.1	24	2	JP0052	ribosomal protein
15	25	18.4	10	2	H37196	bradykinin-potenti
16	25	18.4	15	2	PA0071	superoxide dismuta
17	25	18.4	15	2	I50503	agrin - electric r
18	25	18.4	17	2	D22595	bombolitin IV - Am
19	25	18.4	20	2	PS0028	flagellar motor sw
20	25	18.4	20	2	H28949	ribosomal protein
21	25	18.4	21	2	B33600	glutamate-ammonia
22	25	18.4	22	2	D47256	kinetoplast DNA-as
23	25	18.4	24	2	G85602	hypothetical prote
24	25	18.4	25	2	A60621	somatotropin - Atl
25	24	17.6	10	2	B37196	bradykinin-potenti
26	24	17.6	20	2	S23981	outer layer protei
27	24	17.6	20	2	S46479	retinoid-X-recepto
28	24	17.6	21	2	S51066	ribosomal protein
29	24	17.6	22	2	C42856	hypothetical prote

ALIGNMENTS

RESULT 1

S07770
histone H2B.1, sperm - sea urchin (Echinus esculentus) (fragment)
C:Species: Echinus esculentus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Feb-1997
C:Accession: S07770
R: Hill, C.S.; Thomas, J.O.
Eur. J. Biochem. 187, 145-153, 1990
A:Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal ta:
A:Reference number: S07769; MUID:90126812; PMID:2238202
A:Accession: S07770
A:Molecule type: protein
A:Residues: 1-25 <HIL>
C:Superfamily: histone H2B
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus
Query Match 21.3%; Score 29; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPGKRAP 25

DB 4 KSPTKRSP 11

RESULT 2

S78765
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78765
R: Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: Protein
A:Residues: 1-11 <GRA>
C:Keywords: mitochondrion
F:1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 20.6%; Score 28; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPPLPKDIVR 14

DB 2 HVDVFKDLTK 11

RESULT 3

PHI351
Ig heavy chain DJ region (clone C100-109B) - human (fragment)

cytochrome-b5 redu
hypothetical prote
kinase-related tra
cytochrome-c oxida
hypothetical 1-5K
hypothetical 1-5K
major allergen Myr
Ig heavy chain DJ
histone H2B - mous
superoxide dismuta
carboxylesterase (
Ca2+/calmodulin-de
T cell receptor V-
ATPase R1 subunit
stromelysin (EC 3.
probable acr-2 reg
platelet aggregati

```
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1351
R;Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1351
A;Molecule type: DNA
A;Residues: 1-16 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match      19.9%; Score 27; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      16 IAKAPGKRAP 25
Db      7 IGSTPGAREP 16

RESULT 4
A41439
acid ribonuclease (EC 3.1.1.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C;Accession: A41439
R;Ohgi, K.; Sando, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A;Title: Purification of acid ribonucleases from bovine spleen.
A;Reference number: A41439; MUID:88227899; PMID:3131316
A;Accession: A41439
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <OHG>
C;Keywords: hydrolase

Query Match      19.9%; Score 27; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      5 HPHPKDI 12
Db      9 HLYFPKDL 16

RESULT 5
ZJBPG4
gene J protein - phage G4
C;Species: phage G4
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 28-Jul-2000
C;Accession: A04259
R;Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.
Nature 276, 236-247, 1978
A;Title: Nucleotide sequence of bacteriophage G4 DNA.
A;Reference number: A93200; MUID:79053264; PMID:714153
A;Accession: A04259
A;Molecule type: DNA
A;Residues: 1-25 <GOD>
A;Cross-references: GB:J02454; GB:M10724; GB:M11404; GB:V00657; MID:g15931; PIDN:CAA2401
C;Comment: Gene J protein is one of the structural components of the bacteriophage coat.
C;Superfamily: phage phi-X174 gene J protein
C;Keywords: DNA binding

Query Match      19.9%; Score 27; DB 1; Length 25;
Best Local Similarity 43.8%; Pred. No. 2.5e+03;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      8 LPKDIVRISIAKAPGKR 23
Db      1 MKKSIRRSRSGSKGAP 16
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RESULT 6
A36016
granulocyte inhibitory protein - human
C;Species: Homo sapiens (man)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 30-May-1997
C;Accession: A36016
R;Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990
A;Title: Physicochemical characterization of a polypeptide present in uremic serum that
A;Reference number: A36016; MUID:90349614; PMID:2385596
A;Accession: A36016
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <HOE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match      19.5%; Score 26.5; DB 2; Length 20;
Best Local Similarity 36.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;

Qy      11 DIVR----SIKAPGKRA 24
Db      1 DIVMTSPGTLVSPPGERA 19

RESULT 7
PQ0143
polygalacturonase (EC 3.2.1.15) P26 - evening primrose (fragment)
C;Species: Oenothera organensis (evening primrose)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
C;Accession: PQ0143
R;Brown, S.M.; Crouch, M.L.
Plant Cell 2, 263-274, 1990
A;Title: Characterization of a gene family abundantly expressed in Oenothera organensis
A;Reference number: JQ0992; MUID:9305658; PMID:2152116
A;Accession: PQ0143
A;Molecule type: mRNA
A;Residues: 1-22 <BRO>
A;Experimental source: pollen
C;Comment: This protein is specifically translated in the pollens.
C;Comment: This protein functions by depolymerizing pectin in the cell walls of the pistil
y growing tube.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      19.5%; Score 26.5; DB 2; Length 22;
Best Local Similarity 38.1%; Pred. No. 2.6e+03;
Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy      1 CRVTHPLPKDIVRSTIAKAPG 21
Db      1 CTITNAQL-FDITKYGAKGDG 20

RESULT 8
S32551
glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
C;Accession: S32551; S32550
R;Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 116, 137-146, 1992
A;Title: Glutathione S-transferases of mouse liver: sex-related differences in the expression
A;Reference number: S32548; MUID:92256466; PMID:1581342
A;Accession: S32551
A;Molecule type: protein
A;Residues: 1-13 <SINI>
A;Experimental source: female
A;Accession: S32550
A;Molecule type: protein
A;Residues: 1-13 <SIN2>
A;Experimental source: male
C;Keywords: transferase
```

Query Match 19.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHP 6
 DB 9 RLTHP 13

RESULT 9
 I38336
 hypothetical TEL/MN1 mutant fusion protein type I - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
 C;Accession: I38336
 R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
 Oncogene 10, 1511-1519, 1995
 A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion of TEL and MN1 genes
 A;Reference number: I38031; MUID:95249265; PMID:7731705
 A;Accession: I38336
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-15 <BU1>
 A;Cross-references: EMBL:X85026; NID:g971473; PIDN:CAA59399.1; PID:g971474
 C;Comment: This sequence is the chimeric product of a translocation mutation.
 C;Genetics:
 A;Gene: ERV6/MN1; TEL/MN1
 A;Map position: 22q11/12p13
 C;Keywords: fusion protein

Query Match 19.1%; Score 26; DB 4; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12
 DB 6 HLPDHL 11

RESULT 10
 JP0055
 ribosomal protein L30 - Bacillus polymyxa (fragment)
 C;Species: Bacillus polymyxa
 C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000
 C;Accession: JP0055
 R;Ochi, K.
 submitted to JIPID, February 1994
 A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal protein L30
 A;Reference number: JP0042
 A;Accession: JP0055
 A;Molecule type: protein
 A;Residues: 1-20 <OCH>
 C;Superfamily: Escherichia coli ribosomal protein L30
 C;Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSTIAPG 21
 DB 7 LVRSILIGFG 16

RESULT 11
 H30608
 Ig kappa chain V-III region (Ste) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C;Accession: H30608
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
 J. Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies

A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: H30608
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <GON>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 STAKAPGKRA 24
 DB 10 TLSVSPGERA 19

RESULT 12
 D30609
 IG kappa chain V-III regions (Jon and Mit) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C;Accession: D30609
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
 J. Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: D30609
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <GON>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 STAKAPGKRA 24
 DB 10 TLSVSPGERA 19

RESULT 13
 B30609
 Ig kappa chain V-III region (She) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
 C;Accession: B30609
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
 J. Immunol. 142, 3158-3163, 1989
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A;Reference number: A30601; MUID:89215279; PMID:2496160
 A;Accession: B30609
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <GON>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 STAKAPGKRA 24
 DB 10 TLSVSPGERA 19

RESULT 14
 JP0052
 ribosomal protein L30 - Bacillus macquariensis (fragment)
 C;Species: Bacillus macquariensis

C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 02-Sep-2000
C;Accession: JF0052
R;Ochi, K.
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal protein
A;Reference number: JF0042
A;Accession: JF0052
A;Molecule type: protein
A;Residues: 1-24 <OCH>
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSLIAPG 21
DB 8 LVRSLIGRPG 17

RESULT 15
H37196
bradykinin-potentiating peptide 8 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C;Accession: H37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides B
A;Reference number: A37196; PMID:90351557; PMID:2386615
A;Accession: H37196
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPHLP 9
DB 5 HFNIP 9

Search completed: March 18, 2004, 14:02:08
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:54:34 ; Search time 11 seconds
(without alignments)
118.341 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 1653

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	22.8	18	1	CT1C_LITCI
2	29	21.3	18	1	P81838 litoria cit
3	29	21.3	25	1	P13281 echinus esc
4	27	19.9	12	1	P82619 periplaneta
5	27	19.9	25	1	P03652 bacterioph
6	26.5	19.5	19	1	P81735 leucophaea
7	26	19.1	13	1	P82050 litoria ewi
8	26	19.1	15	1	P80612 zea mays (m
9	26	19.1	16	1	P81840 litoria cit
10	26	19.1	18	1	P81845 litoria cit
11	25	18.4	10	1	P30426 bothrops in
12	25	18.4	13	1	P82386 litoria ran
13	25	18.4	13	1	P82387 litoria ran
14	25	18.4	13	1	P56870 rhodococcus
15	25	18.4	16	1	P81846 litoria cit
16	25	18.4	17	1	P07495 megabombus
17	25	18.4	19	1	P14552 klebsiella
18	25	18.4	20	1	P12740 haloarcula
19	25	18.4	25	1	P56235 litoria cae
20	25	18.4	25	1	P56236 litoria cae
21	24	17.6	10	1	P30422 bothrops in
22	24	17.6	15	1	Q92060 gallus gall
23	24	17.6	16	1	P82389 litoria aur
24	24	17.6	16	1	P82390 litoria aur
25	24	17.6	16	1	P81835 litoria cit
26	24	17.6	16	1	P18638 coturnix co
27	24	17.6	17	1	P82394 litoria ran
28	24	17.6	17	1	P82395 litoria ran
29	24	17.6	17	1	P82396 litoria ran
30	24	17.6	18	1	P81839 litoria cit
31	24	17.6	20	1	Q9pe49 gallus gall
32	24	17.6	23	1	P33177 anabaena sp
33	23	16.9	10	1	P80982 thunnus obe

34 23 16.9 16 1 AU21_LITRA
35 23 16.9 16 1 AU25_LITRA
36 23 16.9 17 1 RS13_PARDE
37 23 16.9 18 1 LVC_ESTAC
38 23 16.9 20 1 MIL7_BOVIN
39 23 16.9 20 1 SODM_HORVU
40 23 16.9 21 1 CFPA_TREPH
41 23 16.9 23 1 SODM_RANCA
42 22 16.2 10 1 GON2_CHEPR
43 22 16.2 16 1 MNPX_SOLTU
44 22 16.2 17 1 H2B3_ICTPU
45 22 16.2 19 1 UP22_UPEIN

ALIGNMENTS

RESULT 1
CT1C_LITCI
ID CT1C_LITCI STANDARD; PRT; 18 AA.
AC P81844;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Citropin 1.2.4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue mountains tree-frog Litoria citropa. Solution structure of the antibacterial peptide citropin 1.1.";
RL Eur. J. Biochem. 265:627-637(1999).
CC -!- SURCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide.
SQ SEQUENCE 18 AA; 1814 MW; 500BF778D515ABD7 CRC64;
Query Match 22.8%; Score 31; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 11 DIVRSIAKAPGKRAP 25
|:::|:::|:::|
Db 4 DIKKVASVVGASLP 18
RESULT 2
CT1A_LITCI
ID CT1A_LITCI STANDARD; PRT; 18 AA.
AC P81838;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Citropin 1.1.3.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;

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RT "Host defence peptides from the skin glands of the Australian blue
RT mountain tree-frog Litoria citropa. Solution structure of the
RT antibacterial peptide citropin 1-11."
RL Eur. J. Biochem. 265:627-637(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide.
SQ SEQUENCE 18 AA; 1814 MW; 500BF778D51F98D7 CRC64;

Query Match 21.3%; Score 29; DB 1; Length 18;
Best Local Similarity 26.7%; Pred. No. 4.3e+02;
Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 11 DIVRSIAKPGKRAP 25
DB 4 DVIKKVASVIGLASP 18

RESULT 3
H2B1_ECHES
ID H2B1_ECHES STANDARD; PRT; 25 AA.
AC P13281;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B-1, sperm (fragment).
OS Echinus esculentus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoides; Euechinoides; Echinacea; Echinoida; Echinidae; Echinus.
OX NCBI_TaxID=7648;
RN [1]
RP SEQUENCE.
RX MEDLINE=90126812; PubMed=2298202;
RA Hill C.S., Thomas J.O.;
RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
RT terminal tail of H2B interacts with linker DNA."
RL Eur. J. Biochem. 187:145-153(1990).
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the histone H2B family.
DR PIR; S07770; S07770.
DR InterPro; IPR000558; Histone H2B.
DR PROSITE; PS00357; HISTONE H2B; PARTIAL.
KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
KW Multigene family.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPGKRAP 25
DB 4 KSPTKRSPP 11

RESULT 4
PPK4_PPRAM
ID PPK4_PPRAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRAL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

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RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach."
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Ragna-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FP42CAA1 CRC64;

Query Match 19.9%; Score 27; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12
DB 2 HLPKDV 7

RESULT 5
VGJ_BPG4
ID VGJ_BPG4 STANDARD; PRT; 25 AA.
AC P03652;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small core protein (J protein).
GN J.
OS Bacteriophage G4.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79053264; PubMed=714153;
RA Godson G.N., Barrell B.G., Staden R., Fiddes J.C.;
RT "Nucleotide sequence of bacteriophage G4 DNA."
RL Nature 276:236-247(1978).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=96217890; PubMed=8642594;
RA McKenna R., Bowman B.R., Liag L.L., Rosemann M.G., Fane B.A.;
RT "Atomic structure of the degraded procapsid particle of the
RT bacteriophage G4: induced structural changes in the presence of
RT calcium ions and functional implications."
RL J. Mol. Biol. 256:736-750(1996).
CC -!- FUNCTION: The J protein is associated with the DNA and is situated
CC in an interior cleft of the P protein.
CC -!- SUBUNIT: The virion is composed of 60 copies each of the F, G, and
CC J proteins, and 12 copies of the H protein.
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EMBL; V00657; CAA24018.1; --
PIR; A04259; ZJBPG4.

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tree frog, Litoria ewingi. Sequence determination and antimicrobial
activity."
Aust. J. Chem. 50:889-894(1997).
-!- FUNCTION: Uperin 7.1 shows antibacterial activity against L.lactis
and S.uberis. Uperin 7.1.1 is inactive.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.
-!- MASS SPECTROMETRY: MW=1184; METHOD=FAB; RANGE=3-13.
KW Amphibian defense peptide; Antibiolic; Amidation.
PEPTIDE 1 13 UPERIN 7.1.1.
FT PEPTIDE 3 13 UPERIN 7.1.1.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1429 MW; DE17C7204CCAE322 CRC64;

Query Match 19.1%; Score 26; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 8.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 DIVRSIATA 19
| | | | |
DB 4 DVVKHIAA 12

RESULT 8
UC06 MAIZE
ID UC06 MAIZE STANDARD; PRT; 15 AA.
AC P806I2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 1131)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.8, its MW is: 71.0 kDa.
DR MAIZE-2DPAGE; P806I2; COLEOPTILE.
DR MaizedB; 123930; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match 19.1%; Score 26; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 AKAPGKRAP 25
| | | | |
DB 2 AAAPPRGP 10

RESULT 9
CT12 LITCI
ID CT12 LITCI STANDARD; PRT; 16 AA.
AC P81840; P81841; P81842; P81843;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Citropin 1.2 [Contains: Citropin 1.2.1; Citropin 1.2.2; Citropin
DE 1.2.3].
DE Litoria citropa (Australian blue mountains tree frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog *Litoria citropa*. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -!- FUNCTION: Bacteriostatic action for Gram-positive bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT PEPTIDE 1 16
 FT CITROPIN 1.2.1.
 FT PEPTIDE 3 14
 FT CITROPIN 1.2.2.
 FT PEPTIDE 4 14
 FT CITROPIN 1.2.3.
 FT PEPTIDE 1 11
 FT CITROPIN 1.2.3.
 FT MOD_RES 16 16
 FT AMIDATION.
 SQ SEQUENCE 16 AA; 1616 MW; 1D878515ABD73DE9 CRC64;

 Query Match 19.1%; Score 26; DB 1; Length 16;
 Best Local Similarity 36.4%; Pred. No. 1e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 Qy 11 DIVRSIAKAPG 21
 Db 4 DIIRKVASWG 14

 RESULT 10
 CTID LITCI STANDARD; PRT; 18 AA.
 ID CTID LITCI STANDARD; PRT; 18 AA.
 AC P81845;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Citropin 1.2.5.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 RA Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog *Litoria citropa*. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
 KW Amphibian defense peptide.
 SQ SEQUENCE 18 AA; 1845 MW; 51BBF778D515ABD7 CRC64;

 Query Match 19.1%; Score 26; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

 Qy 11 DIVRSIAKAPG 21
 Db 4 DIIRKVASWG 14

 RESULT 11
 BPP8 BOTIN STANDARD; PRT; 10 AA.
 ID BPP8 BOTIN STANDARD; PRT; 10 AA.

AC P30426;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5.1 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Iland jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from *Bothrops insularis* snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 CC PIR; H37196; H37196.
 DR Hypotensive agent; Pyrrolidone carboxylic acid.
 KW MOD_RES 1 1
 FT PYRROLIDONE CARBOXYLIC ACID.
 FT SEQUENCE 10 AA; 1173 MW; 2FF83545761F6D8 CRC64;

 Query Match 18.4%; Score 25; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 9e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 HPHLP 9
 Db 5 HENIP 9

 RESULT 12
 AU11 LITRA STANDARD; PRT; 13 AA.
 ID AU11 LITRA STANDARD; PRT; 13 AA.
 AC P82386;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Aurein 1.1.
 OS Litoria raniformis (Southern bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=116057;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rizek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs *Litoria aurea* and *Litoria raniformis* the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -!- FUNCTION: Antimicrobial activity against *B.cereus*, *L.lactis*,
 CC *L.monococcus* and *S.suberis*. Probably acts by disturbing membrane
 CC functions with its amphipathic structure.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT MOD_RES 13 13
 FT AMIDATION.
 SQ SEQUENCE 13 AA; 1447 MW; 173CB99DF8C83330 CRC64;

 Query Match 18.4%; Score 25; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;


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QY 11 DIVRSIAXA 19
Db 4 DLIKKIAES 12

RESULT 13
AUI2_LITRA STANDARD; PRT; 13 AA.
AC P82387;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aurein 1.2.
OS Litoria raniformis (Southern bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=116057;
RN [1]
RP SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
PT "The antibiotic and anticancer active aurein peptides from the
RT australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: Antimicrobial activity against B.cereus, L.lactis,
CC L.innocua, M.luteus, P.multocida, S.aureus, S.epidermidis and
CC S.suberis. Probably acts by disturbing membrane functions with its
CC amphipathic structure. Shows anticancer activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC KW Amphibian defense peptide; Amidation; Antibiotic.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1481 MW; 1EACB99DFBC83330 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 11 DIVRSIAXA 19
Db 4 DLIKKIAES 12

RESULT 14
MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=1CP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus 1CP."
RL J. Bacteriol. 180:3503-3508(1998).
CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +
CC NAD(P)H.
CC -!- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
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CC -!- SIMILARITY: Belongs to the iron-containing alcohol dehydrogenase
CC family.
DR InterPro: IPR001670; Fe-ADH.
DR PROSITE: PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE: PS00080; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON TER 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 18.4%; Score 25; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDI 12
Db 2 RFEHENLPQRI 12

RESULT 15
CT13_LITCI STANDARD; PRT; 16 AA.
AC P81846;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Citropin 1.3.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;
PT "Host defence peptides from the skin glands of the Australian blue
RT mountains tree-frog Litoria citropa. Solution structure of the
RT antibacterial peptide citropin 1.1."
RL Eur. J. Biochem. 265:627-637(1999).
CC -!- FUNCTION: Bacteriostatic action for Gram-positive bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 16
SQ SEQUENCE 16 AA; 1630 MW; 1D8785073BD73DE9 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 DIVRSIAXAPG 21
Db 4 DLIKKVASVIG 14

Search completed: March 18, 2004, 14:00:44
Job time : 12 secs
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:57:54 ; Search time 38 Seconds
(without alignments)
207.578 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 11070

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	22.1	18	4	Q9BQT0
2	30	22.1	19	15	Q90RH8
3	30	22.1	20	11	Q99JV2
4	29	21.3	16	8	Q9T2R0
5	29	21.3	19	4	Q15271
6	28	20.6	22	7	Q9MX47
7	28	20.6	24	2	Q9L7N8
8	27	19.9	15	4	Q9UEM3
9	27	19.9	20	4	Q9UM18
10	27	19.9	21	6	Q9NCJ5
11	27	19.9	24	10	Q7XAX3
12	26.5	19.5	17	5	Q9TWR3
13	26.5	19.5	22	10	Q9S9B8
14	26	19.1	15	4	Q9UCJ8
15	26	19.1	16	8	Q9T2V8
16	26	19.1	18	6	Q95JA2

17	19.1	26	21	12	Q85667
18	26	26	24	2	Q9L7N6
19	26	26	25	11	Q9QUW9
20	25.5	18.8	16	6	Q9TRD1
21	25.5	18.8	24	5	Q9U542
22	25	18.4	13	2	Q8GBU2
23	25	18.4	14	3	P90342
24	25	18.4	15	13	Q90403
25	25	18.4	17	6	Q9XSG1
26	25	18.4	18	2	Q9RAE0
27	25	18.4	19	13	Q42416
28	25	18.4	19	15	Q90RH4
29	25	18.4	21	4	Q9H4Z8
30	25	18.4	22	5	Q9TWU8
31	25	18.4	22	13	Q9PS65
32	25	18.4	23	2	Q43887
33	25	18.4	23	5	Q95S95
34	25	18.4	23	10	Q94IS9
35	25	18.4	24	2	Q9KIL6
36	25	18.4	24	16	Q8XAG7
37	25	18.4	25	10	Q94IS2
38	25	18.4	25	12	Q80J46
39	25	18.4	25	12	Q80J44
40	25	18.4	25	12	Q80J43
41	24.5	18.0	20	13	Q9PSH5
42	24.5	18.0	25	6	Q8MI11
43	24	17.6	13	8	Q33417
44	24	17.6	15	11	Q9QV01
45	24	17.6	17	2	Q34216

ALIGNMENTS

RESULT 1

Q9BQT0 ID Q9BQT0 PRELIMINARY; PRT; 18 AA.
AC Q9BQT0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21195339; PubMed=11297743;
RA Holzmann K., Ambrosch I., Elbling L., Micksche M., Berger W.;
RT "A small upstream open reading frame causes inhibition of human major
RT vault protein expression from a ubiquitous mRNA splice variant.";
RL FEBS Lett. 494:99-104(2001).
DR EMBL; AJ291367; CAC35315.1; -.
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 22.1%; Score 30; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRVTHPLP 9
||: ||||
Db 8 CRL--PHLP 14

RESULT 2

Q90RH8 ID Q90RH8 PRELIMINARY; PRT; 19 AA.
AC Q90RH8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

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DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG12;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF127545; AAK84896.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;

Query Match 22.1%; Score 30; DB 15; Length 19;
Best Local Similarity 53.8%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 PHLPKDIVRSIAK 18
Db 7 PHSSKDHQNSIPK 19

RESULT 3
Q99JV2 PRELIMINARY; PRT; 20 AA.
AC Q99JV2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005653; AAH05653.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2223 MW; F203F6A80A7A0429 CRC64;

Query Match 22.1%; Score 30; DB 11; Length 20;
Best Local Similarity 70.0%; Pred. No. 2e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 VRSIAKAPGK 22
Db 1 VFSAAKRPCK 10

RESULT 4
Q97R0 PRELIMINARY; PRT; 16 AA.
AC Q97R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome-C reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).
OS Solanum tuberosum (Potato).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]

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RP SEQUENCE.
RX MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
DR GO: GO:0008121; F:ubiquinol-cytochrome-c reductase activity; IEA.
SQ SEQUENCE 16 AA; 1946 MW; BBC625F8E4A4C8E7 CRC64;

Query Match 21.3%; Score 29; DB 8; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 HPPLPKDJI 12
Db 2 HQYLPEDL 9

RESULT 5
Q16271 PRELIMINARY; PRT; 19 AA.
AC Q16271;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine vasopressin V2 receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Holtzman E.J., Kolakowski L.F.Jr., Geifman-Holtzman O., O'Brien D.G.,
RA Rasoulpour M., Guillot A.P., Ausiello D.A.;
RT "Mutations in the vasopressin V2 receptor gene in two families with
RT nephrogenic diabetes insipidus.";
RL J. Am. Soc. Nephrol. 5:169-176(1994).
DR EMBL: S75754; AAB32753.1; -.
KW Receptor.
DR GO: GO:0004872; F:receptor activity; IEA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 1905 MW; 181640EFD90F2788 CRC64;

Query Match 21.3%; Score 29; DB 4; Length 19;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 5 HPPLPKDIVRSIAKAP 20
Db 4 HPSLPSCAWASLSAQP 19

RESULT 6
Q9MX47 PRELIMINARY; PRT; 22 AA.
AC Q9MX47;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class II antigen (Fragment).
GN ORLA-DCB.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HNI;
RA Naruse K., Oku H., Kojima A., Bessho Y., Kuroda N., Matsuzaki T.,
RA Hori H., Shima A., Nonaka M.;
RT "Molecular cloning and linkage analysis of medaka fish MHC class II B
RT genes.";

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RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033216; BAA94283.1; -.
 FT InterPro; IPR007110; IG-Ilike.
 FT NON_TER 1
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2441 MW; E2AFIA9CD581F5FB CRC64;

Query Match 20.6%; Score 28; DB 7; Length 22;
 Best Local Similarity 38.5%; Pred. No. 4.4e+03;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIV 13
 ||| : : :
 Db 7 CRVHVSLKDLPI 19

RESULT 7
 Q9L7N8 PRELIMINARY; PRT; 24 AA.
 AC Q9L7N8; (1)
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE BmpD (Fragment).
 GN BmpD.
 OS Borrelia afzelii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OC NCBI_TaxID=29518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ip3;
 RX MEDLINE=20179823; PubMed=10715014;
 RA Gorbacheva V.Y., Godfrey H.P., Cabello F.C.;
 RT "Analysis of the bnp gene family in Borrelia burgdorferi sensu lato."
 RL J. Bacteriol. 182:2037-2042(2000).
 DR EMBL; AF222435; AAF45174.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 24 AA; 2681 MW; 57F3887CDS9126F9 CRC64;

Query Match 20.6%; Score 28; DB 2; Length 24;
 Best Local Similarity 46.2%; Pred. No. 4.9e+03;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 12 IVESIAKAPGKRA 24
 ||| : : : : :
 Db 1 IINGIIKAPYDKA 13

RESULT 8
 Q9UEM3 PRELIMINARY; PRT; 15 AA.
 AC Q9UEM3; (1)
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Axonal dynein, heavy chain (Fragment).
 GN DNAH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maiti A.K., Mattei M.G., Jorissen M., Volz A., Ziegler A.,
 RA Bouvagnet P.;
 RT "Chromosomal localization of human dynein heavy chain genes."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ132092; CAA10565.1; -.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1646 MW; 4EDFDA937C826170 CRC64;

Query Match 19.9%; Score 27; DB 4; Length 15;

Best Local Similarity 44.4%; Pred. No. 4.2e+03;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 10 KDIVERSIAK 18
 ||| : : : : :
 Db 6 KDLAKALAK 14

RESULT 9
 Q9UMI8 PRELIMINARY; PRT; 20 AA.
 AC Q9UMI8; (1)
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mucin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89235154; PubMed=2715633;
 RA Xing P.X., Tjandra J.J., Reynolds K., McLaughlin P.J., Purcell D.F.J.,
 RA McKenzie I.F.C.;
 RT "Reactivity of anti-human milk fat globule antibodies with synthetic
 RT peptides."
 RL J. Immunol. 142:3503-3509(1989).
 DR EMBL; M26316; AAA36336.1; -.
 DR PIR; S10571; S10571.1
 FT NON_TER 1
 FT NON_TER 20
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 1887 MW; 5B3473EABAFAD87 CRC64;

Query Match 19.9%; Score 27; DB 4; Length 20;
 Best Local Similarity 71.4%; Pred. No. 5.7e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 AFGKRAP 25
 ||| : : : : :
 Db 6 ARGSTAP 12

RESULT 10
 Q9NOJ5 PRELIMINARY; PRT; 21 AA.
 AC Q9NOJ5; (1)
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Choline acetyltransferase (Fragment).
 GN CHAT.
 OS Saguinus imperator (Emperor tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OC NCBI_TaxID=9491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mumbilla M.V.;
 RT "CHAT Gene evolution in the mammalian genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ276478; CAB77548.1; -.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 21
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2255 MW; CB5D0293BC3B05AF CRC64;

Query Match 19.9%; Score 27; DB 6; Length 21;
 Best Local Similarity 46.7%; Pred. No. 5.9e+03;
 Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 6 PHLPKDIVRSIAKAP 20
 ||| : : : : :
 Db 6 PHLPKDIVRSIAKAP 20

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Db 2 PILGKOPHKAAKTP 16
RESULT 11
ID Q7XAX3 PRELIMINARY; PRT; 24 AA.
AC Q7XAX3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Terpene synthase (Fragment)
OS Brassica rapa subsp. pekinensis (Chinese cabbage) (Celery cabbage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=51351;
RN [1]
RP SEQUENCE FROM N.A.
RA Park Y.-S., Cho T.-J.;
RT "Characterization of methyl jasmonate-inducible genes in Chinese
cabbage."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY337005; AAQ01569.1;
FT NON TER 1
SQ SEQUENCE 24 AA; 2887 MW; DCBA1747748690A6 CRC64;

Query Match 19.9%; Score 27; DB 10; Length 24;
Best Local Similarity 38.5%; Pred. No. 6.8e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 THPHLPKDIVRSI 16
||| | | |
Db 5 THPEFLKEHIVSL 17

RESULT 12
Q9TWR3 PRELIMINARY; PRT; 17 AA.
AC Q9TWR3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Histone H1 (Fragment)
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE.
RX MEDLINE=94043510; PubMed=8227175;
RA Toro G.C., Gallanti N., Hellman U., Wernstedt C.;
RT "Unambiguous identification of histone H1 in Trypanosoma cruzi."
RL J. Cell. Biochem. 52:431-439(1993).
SQ SEQUENCE 17 AA; 1820 MW; AD19BC52D8ECCD5 CRC64;

Query Match 19.5%; Score 26.5; DB 5; Length 17;
Best Local Similarity 40.0%; Pred. No. 5.7e+03;
Matches 6; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 9 PKDIVRSIAKAPGR 23
||| | | | |
Db 6 PK---KAVKAPKPK 17

RESULT 13
Q9S9B8 PRELIMINARY; PRT; 22 AA.
AC Q9S9B8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Polygalacturonase homolog (Fragment)
OC Cenothea organensis (Evening primrose).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Onagraceae; Oenothera.
OX NCBI_TaxID=3945;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93005658; PubMed=2152116;
RA Brown S.M., Crouch M.L.;
RT "Characterization of a gene family abundantly expressed in Oenothera
organensis pollen that shows sequence similarity to
RT polygalacturonase."
RL Plant Cell 2:263-274(1990).
DR PIR; P00143; P00143.
SQ SEQUENCE 22 AA; 2289 MW; 2383FFEB1F3CC70 CRC64;

Query Match 19.5%; Score 26.5; DB 10; Length 22;
Best Local Similarity 38.1%; Pred. No. 7.4e+03;
Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDIVRSIAKAPG 21
||| | | | |
Db 1 CTITNAQL-FDITKYGAKGDG 20

RESULT 14
Q9UCJ8 PRELIMINARY; PRT; 15 AA.
AC Q9UCJ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Type IV PROCOLLAGENASE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93125366; PubMed=1480041;
RA Stetler-Stevenson W.G., Kruttsch H.C., Liotta L.A.;
RT "TIMP-2: identification and characterization of a new member of the
RT metalloproteinase inhibitor family."
RL Matrix Suppl. 1:299-306(1992).
SQ SEQUENCE 15 AA; 1537 MW; D5DA1AAA9C32276C CRC64;

Query Match 19.1%; Score 26; DB 4; Length 15;
Best Local Similarity 60.0%; Pred. No. 5.9e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 16 IAKAPGKRAP 25
||| | | | |
Db 5 IIKFPGDVAP 14

RESULT 15
Q9T2V8 PRELIMINARY; PRT; 16 AA.
AC Q9T2V8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2-enoyl-CoA hydratase (Fragment)
OS Homo sapiens (Human)
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95046784; PubMed=7958339;
RX Middleton B.;
RT "The mitochondrial long-chain trifunctional enzyme: 2-enoyl-CoA
RT hydratase, 3-hydroxyacyl-CoA dehydrogenase and 3-oxoacyl-CoA
RT thiolase.";
```

RL Biochem. Soc. Trans. 22:427-431(1994).
 DR GO:0005739; C-mitochondrion; NAS.
 DR GO:0004300; F-acyl-CoA hydratase activity; NAS.
 DR GO:0006835; P-fatty acid beta-oxidation; NAS.
 SQ SEQUENCE 16 AA; 1763 MW; 31AD66A3080B019A CRC64;
 Query Match 19.1%; Score 26; DB 8; Length 16;
 Best Local Similarity 31.2%; Pred. No. 6.3e+03;
 Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 10 KDIVRSIAKAPGRAP 25
 | : : : | | |
 Db 1 KPNIRNVVVVDGVRTP 16

Search completed: March 18, 2004, 14:01:36
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 18, 2004, 14:01:40 ; Search time 39 Seconds
(without alignments)

165.997 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 214167

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	25	9	US-09-938-700-4
2	89	65.4	17	15	US-10-325-375A-2
3	72	52.9	17	15	US-10-325-375A-4
4	69	50.7	17	15	US-10-325-375A-3
5	65	47.8	17	15	US-10-325-375A-6
6	61	44.9	17	15	US-10-325-375A-5
7	60	44.1	14	12	US-10-362-527-313
8	60	44.1	14	12	US-10-304-443-107
9	60	44.1	16	14	US-10-304-443-97
10	60	44.1	16	14	US-10-304-443-120
11	60	44.1	18	12	US-10-362-527-315
12	60	44.1	18	12	US-10-362-527-321
13	60	44.1	18	14	US-10-304-443-98
14	60	44.1	18	14	US-10-304-443-109
15	60	44.1	18	14	US-10-304-443-115

16	60	44.1	18	14	US-10-304-443-121	Sequence 121, App
17	60	44.1	20	12	US-10-362-527-316	Sequence 316, App
18	60	44.1	20	12	US-10-362-527-322	Sequence 322, App
19	60	44.1	20	14	US-10-304-443-110	Sequence 110, App
20	60	44.1	20	14	US-10-304-443-116	Sequence 116, App
21	60	44.1	25	9	US-09-974-449-33	Sequence 33, Appl
22	56	41.2	14	14	US-10-304-443-96	Sequence 96, Appl
23	56	41.2	14	14	US-10-304-443-119	Sequence 119, Appl
24	56	41.2	16	12	US-10-362-527-314	Sequence 314, App
25	56	41.2	16	12	US-10-362-527-320	Sequence 320, App
26	56	41.2	16	14	US-10-362-527-320	Sequence 108, App
27	56	41.2	16	14	US-10-304-443-108	Sequence 114, App
28	55	40.4	19	12	US-10-362-527-62	Sequence 62, Appl
29	55	40.4	19	14	US-10-322-210-3	Sequence 3, Appl
30	55	40.4	19	14	US-10-304-443-3	Sequence 3, Appl
31	51	37.5	12	14	US-10-304-443-95	Sequence 95, Appl
32	51	37.5	13	12	US-10-362-527-77	Sequence 77, Appl
33	51	37.5	13	14	US-10-322-210-18	Sequence 18, Appl
34	51	37.5	13	14	US-10-304-443-18	Sequence 94, Appl
35	45	33.1	10	14	US-10-304-443-94	Sequence 312, App
36	45	33.1	12	12	US-10-362-527-312	Sequence 106, App
37	45	33.1	12	14	US-10-304-443-106	Sequence 43303, A
38	44	32.4	20	9	US-09-864-761-43303	Sequence 76, Appl
39	42	30.9	12	12	US-10-362-527-76	Sequence 17, Appl
40	42	30.9	12	14	US-10-322-210-17	Sequence 17, Appl
41	42	30.9	12	14	US-10-304-443-17	Sequence 8, Appl
42	42	30.9	16	15	US-10-325-375A-8	Sequence 93, Appl
43	41	30.1	8	14	US-10-304-443-93	Sequence 311, App
44	41	30.1	10	12	US-10-362-527-311	Sequence 105, App
45	41	30.1	10	14	US-10-304-443-105	

ALIGNMENTS

RESULT 1
US-09-938-700-4
; Sequence 4, Application US/09938700
; Patent No. US20020064525A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, et al.
; TITLE OF INVENTION: Anti-IgE Vaccines
; FILE REFERENCE: PC10761A
; CURRENT APPLICATION NUMBER: US/09/938,700
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE
US-09-938-700-4

Query Match 100.0%; Score 136; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGKRAP 25
Db 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

RESULT 2
US-10-325-375A-2
; Sequence 2, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E

```
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-2

Query Match          65.4%; Score 89; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
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Db 2 CRVTHPLPKDIVRSI 17

RESULT 3
US-10-325-375A-4
; Sequence 4, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-4

Query Match          52.9%; Score 72; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 15
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 16

RESULT 4
US-10-325-375A-3
; Sequence 3, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-3

Query Match          50.7%; Score 69; DB 15; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0046;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 15
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 16

RESULT 5
US-10-325-375A-6
; Sequence 6, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-6

Query Match          47.8%; Score 65; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.017;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 17

RESULT 6
US-10-325-375A-5
; Sequence 5, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-5

Query Match          44.9%; Score 61; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.064;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
   |||||:|||||
```


Db 2 CKVTHEDPLVIVRSI 17

RESULT 7
US-10-362-527-313
; Sequence 313, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide
US-10-362-527-313

Query Match 44.1%; Score 60; DB 12; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.072;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13
| | | | | : :
Db 1 CRVTHPLPALM 13

RESULT 8
US-10-304-443-107
; Sequence 107, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-107

Query Match 44.1%; Score 60; DB 14; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.072;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13
| | | | | : :
Db 1 CRVTHPLPALM 13

RESULT 9
US-10-304-443-97
; Sequence 97, Application US/10304443

; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human peptide sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (2)
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids
US-10-304-443-97

Query Match 44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.084;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRS 15
| | | | | : :
Db 3 RVTHPLPALMRS 16

RESULT 10
US-10-304-443-120
; Sequence 120, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-120

Query Match 44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.084;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRS 15
| | | | | : :
Db 3 RVTHPLPALMRS 16

RESULT 11
US-10-362-527-315
; Sequence 315, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236

; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide
; NAME/KEY: VARIANT
; LOCATION: (1)...(18)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-362-527-315

Query Match 44.1%; Score 60; DB 12; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.095; 1; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15
| | | | | | | | | | | | | | | | | |
Db 4 RVTHPHLPALMRS 17

RESULT 12
US-10-362-527-321
; Sequence 321, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide
US-10-362-527-321

Query Match 44.1%; Score 60; DB 12; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.095; 1; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15
| | | | | | | | | | | | | | | | | |
Db 4 RVTHPHLPALMRS 17

RESULT 13
US-10-304-443-98
; Sequence 98, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.

; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 98
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human peptide sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (3)
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids
US-10-304-443-98

Query Match 44.1%; Score 60; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.095; 3; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15
| | | | | | | | | | | | | | | | | |
Db 4 RVTHPHLPALMRS 17

RESULT 14
US-10-304-443-109
; Sequence 109, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human peptide sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (3)
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids
US-10-304-443-109

Query Match 44.1%; Score 60; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.095; 3; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15
| | | | | | | | | | | | | | | | | |
Db 4 RVTHPHLPALMRS 17

RESULT 15
US-10-304-443-115
; Sequence 115, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A

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; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-115

Query Match      44.1%; Score 60; DB 14; Length 18;
Best Local Similarity 71.4%; Pred.No. 0.895;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 RVTHPHLPKDIVRS 15
Db      4 RVTHPHLPKDIVRS 17

Search completed: March 18, 2004, 14:07:04
Job time : 39 secs
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:59:24 ; Search time 23 Seconds
(without alignments)

56.115 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 191815

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	47.1	25	3	US-09-100-414B-95
2	64	47.1	25	3	US-09-303-323-95
3	64	47.1	25	4	US-09-770-014-95
4	60	44.1	22	2	US-08-232-539D-19
5	60	44.1	24	2	US-08-232-539D-20
6	36	26.5	18	2	US-09-017-205-52
7	36	26.5	22	2	US-08-455-079-18
8	36	26.5	23	2	US-08-455-079-14
9	35.5	26.1	22	1	US-07-988-925-12
10	35.5	26.1	22	2	US-08-362-780-12
11	35	25.7	22	3	US-09-046-985-4
12	35	25.7	22	3	US-09-474-743-4
13	35	25.7	23	3	US-08-851-843A-208
14	35	25.7	23	3	US-08-974-549A-327
15	35	25.7	23	3	US-08-854-050-208
16	35	25.7	23	4	US-09-430-323-208
17	35	25.7	23	4	US-09-402-181B-327
18	35	25.7	23	4	US-09-721-456-327
19	34	25.0	12	2	US-08-323-686-15
20	34	25.0	21	2	US-08-480-190-80
21	34	25.0	21	2	US-08-488-379-80
22	34	25.0	21	4	US-08-475-399A-80
23	34	25.0	21	5	PCT-US93-07545-80
24	32	23.5	20	1	US-07-678-974D-17
25	32	23.5	20	2	US-08-945-168-22
26	32	23.5	24	2	US-08-818-253-15
27	32	23.5	24	3	US-08-818-252-15

28	32	23.5	24	4	US-08-842-322-9	Sequence 9, Appl
29	32	23.5	24	4	US-09-316-919-31	Sequence 31, Appl
30	31.5	23.2	15	2	US-08-934-222-87	Sequence 87, Appl
31	31.5	23.2	15	2	US-08-933-402-87	Sequence 87, Appl
32	31.5	23.2	15	2	US-09-207-621-87	Sequence 87, Appl
33	31.5	23.2	15	2	US-08-532-818-87	Sequence 87, Appl
34	31.5	23.2	15	3	US-09-231-797-87	Sequence 87, Appl
35	31.5	23.2	15	3	US-08-934-224-87	Sequence 87, Appl
36	31.5	23.2	15	3	US-08-933-843-87	Sequence 87, Appl
37	31.5	23.2	15	3	US-08-934-223-87	Sequence 87, Appl
38	31.5	23.2	15	3	US-09-413-492-87	Sequence 103, App
39	31	22.8	14	5	PCT-US93-06751-103	Sequence 5, Appl
40	31	22.8	15	2	US-08-455-079-5	Sequence 9, Appl
41	31	22.8	22	1	US-08-148-209A-9	Sequence 21, Appl
42	31	22.8	24	3	US-08-592-500-27	Sequence 27, Appl
43	31	22.8	24	3	US-08-195-006-27	Sequence 27, Appl
44	31	22.8	24	5	PCT-US94-07644A-27	Sequence 37, Appl
45	30.5	22.4	18	4	US-09-390-134B-37	

ALIGNMENTS

RESULT 1
US-09-100-414B-95
; Sequence 95, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RVTHPLPKDIVRSIAK 18

Db 8 RVTHPLPKALMRSTTK 24

RESULT 2

```

US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-95
;
Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
|||||: :|||
Db 8 RVTHPLPALMRSTTK 24

RESULT 3
US-09-770-014-95
; Sequence 95, Application US/09770014
; Patent No. 6559282
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,014
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-770-014-95
;
Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
|||||: :|||
Db 8 RVTHPLPALMRSTTK 24

RESULT 4
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-770-014-95
;
Query Match 47.1%; Score 64; DB 4; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
|||||: :|||
Db 8 RVTHPLPALMRSTTK 24

RESULT 4
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-770-014-95
;

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US-08-232-539D-19

Query Match 44.1%; Score 60; DB 2; Length 22;
Best Local Similarity 69.2%; Pred. No. 0.0075;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13
|||||: :
DB 10 CRVTHPLPALM 22

RESULT 5

US-08-232-539D-20
; Sequence 20, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:

; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: IGE Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-Apr-1994
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/952-9881

; TELEFAX: 650/225-1489

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 24 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-232-539D-20

Query Match 44.1%; Score 60; DB 2; Length 24;
Best Local Similarity 69.2%; Pred. No. 0.0083;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13
|||||: :
DB 12 CRVTHPLPALM 24

RESULT 6

US-09-017-205-52

; Sequence 52, Application US/09017205
; Patent No. 5965357
; GENERAL INFORMATION:

; APPLICANT: Marsden, Howard S

; TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN

; TITLE OF INVENTION: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2

; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Nixon & Vanderhye PC

; STREET: 8th Floor, 1100 No. 5965357th Glebe Road

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/017,205

; FILING DATE: 02-FEB-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Mitchard, Leonard C

; REGISTRATION NUMBER: 29,009

; REFERENCE/DOCKET NUMBER: 604-436

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)816-4000

; TELEFAX: (703)816-4100

; INFORMATION FOR SEQ ID NO: 52:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide from HSV-2 glycoprotein G

; FRAGMENT TYPE: internal

US-09-017-205-52

Query Match 26.5%; Score 36; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 THPHLPKD 11

DB 7 THPHGPAD 14

RESULT 7

US-08-455-079-18

; Sequence 18, Application US/08455079

; Patent No. 5994292

; GENERAL INFORMATION:

; APPLICANT: Tosato, Giovanna;

; APPLICANT: Angiolillo, Anne L.; Sgadari, Cecilia

; TITLE OF INVENTION: INTERFERON-INDUCIBLE

; TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF

; TITLE OF INVENTION: ANGIOGENESIS

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5-INCH, 1.44 MB STORAGE

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/455,079

; FILING DATE: 31-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KATHRYN M. BROWN

; REGISTRATION NUMBER: 34,556

; REFERENCE/DOCKET NUMBER: 2026-4182

; TELECOMMUNICATION INFORMATION:


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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-362-780-12

Query Match 26.1%; Score 35.5; DB 2; Length 22;
Best Local Similarity 35.0%; Pred. No. 52;
Matches 7; Conservative 5; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPLPKDIVRSIAKAPGK 22
Db :||| |:::|||
4 LTQPH-----SVSESPGK 16

RESULT 11
US-09-046-985-4
; Sequence 4, Application US/09046985
; Patent No. 6121236
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,985
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 130
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; OTHER INFORMATION: /note= "N-Acetyl Alanine"
; US-09-046-985-4

Query Match 25.7%; Score 35; DB 3; Length 22;
Best Local Similarity 40.0%; Pred. No. 63;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HLPKDIVRSIAKAPG 21
Db :||| :|||
8 HRPKDYLSIVRRADG 22

RESULT 12
US-09-474-743-4
; Sequence 4, Application US/09474743
; Patent No. 6235716
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/474,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,985
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; OTHER INFORMATION: /note= "N-Acetyl Alanine"
; US-09-474-743-4

Query Match 25.7%; Score 35; DB 3; Length 22;
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Best Local Similarity 40.0%; Pred. No. 63;
Matches 6; Conservative 3; Mismatches 0;

6; Indels 0; Gaps 0;

QY 7 HLPKDIVRSIAKPG 21
DB 8 HRPKDLVSIVRRADG 22

RESULT 13
US-08-851-843A-208
; Sequence 208, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-851-843A-208

Query Match 25.7%; Score 35; DB 3; Length 23;
Best Local Similarity 38.5%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY 4 THPH---LPKDIVRSIAKPGKRAP 25
DB 6 TSPHPRENLPQD-----FGPRCP 23

RESULT 14

US-08-974-549A-327
; Sequence 327, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0026100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 327:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-327
Query Match      25.7%; Score 35; DB 3; Length 23;
Best Local Similarity 38.5%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY  4 THPH-----LPKDIVRSIAKAPGKRAP 25
    |||||
Db   6 TSPHPRENLPQD-----PGPRCP 23

RESULT 15
US-08-854-050-208
; Sequence 208, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: peptide
US-08-854-050-208
Query Match      25.7%; Score 35; DB 3; Length 23;
Best Local Similarity 38.5%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY  4 THPH-----LPKDIVRSIAKAPGKRAP 25
    |||||
Db   6 TSPHPRENLPQD-----PGPRCP 23

Search completed: March 18, 2004, 14:02:44
Job time : 24 secs
```

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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:53:59 ; Search time 53 Seconds
(without alignments)
133.277 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 546957

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	75.0	20	2	AAW24102 Canine im
2	89	65.4	17	3	AAY50894 Antibody
3	89	65.4	17	3	AAY50893 Antibody
4	89	65.4	25	3	AAY79999 Optimised
5	79	58.1	20	2	AAW24103 Canine im
6	72	52.9	17	3	AAY50896 Antibody
7	69	50.7	17	3	AAY50895 Antibody
8	68	50.0	25	3	AAY80000 Optimised
9	65	47.8	17	3	AAY50898 Antibody
10	64	47.1	25	3	AAY68602 Peptide s
11	64	47.1	25	3	AAY91212 Modified
12	64	47.1	25	3	AAY79998 Optimised
13	63	46.3	25	3	AAY80077 Optimised
14	61	44.9	17	3	AAY50897 Antibody
15	60	44.1	14	5	AAO18028 Human imm
16	60	44.1	14	5	ABJ00529 Human IGE
17	60	44.1	16	5	AAO18018 Human imm
18	60	44.1	16	5	AAO18041 Human imm
19	60	44.1	18	5	AAO18030 Human imm
20	60	44.1	18	5	AAO18019 Human imm
21	60	44.1	18	5	AAO18042 Human imm
22	60	44.1	18	5	AAO18036 Human imm
23	60	44.1	18	5	ABJ00531 Human IGE
24	60	44.1	18	5	ABJ00537 Human IGE
25	60	44.1	20	5	AAO18031 Human imm

26	60	44.1	20	5	AAO18037 Human imm
27	60	44.1	20	5	ABJ00532 Human IGE
28	60	44.1	20	5	ABJ00538 Human IGE
29	60	44.1	22	2	AAY42585 IGE pepti
30	60	44.1	24	2	AAY42586 IGE pepti
31	57	41.9	17	2	AAR02179 Peptide w
32	56	41.2	14	5	AAO18040 Human imm
33	56	41.2	14	5	AAO18017 Human imm
34	56	41.2	16	5	AAO18035 Human imm
35	56	41.2	16	5	AAO18029 Human imm
36	56	41.2	16	5	ABJ00536 Human IGE
37	56	41.2	16	5	ABJ00530 Human IGE
38	55	40.4	19	3	AAB26503 Human IGE
39	55	40.4	19	4	AAB51033 IGE pepti
40	55	40.4	19	4	AAU16830 Peptide P
41	55	40.4	19	5	ABJ00278 Human IGE
42	51	37.5	12	5	AAO18016 Human imm
43	51	37.5	13	3	AAB26518 Human IGE
44	51	37.5	13	4	AAU16849 Peptide P
45	51	37.5	13	5	ABJ00293 Human IGE

ALIGNMENTS

RESULT 1

AAW24102
ID: AAW24102 standard; peptide; 20 AA.
XX
AC AAW24102;
XX
DT 21-NOV-1997 (first entry)
XX
DE Canine immunoglobulin E peptide 5.
XX
KW Immunoglobulin E; IGE; anti-canine IGE antibody; allergy; canine; dog.
XX
OS Canis familiaris.
XX
PN JP09169795-A.
XX
PD 30-JUN-1997.
XX
PF 22-DEC-1995; 95JP-00334381.
XX
PR 22-DEC-1995; 95JP-00334381.
XX
(HITB) HITACHI CHEM CO LTD.
XX
DR WPI; 1997-389423/36.
XX
N-PSDB; AAT85651.
XX
PT Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.
XX
PS Claim 2; Page 9; 12pp; Japanese.
XX

CC AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IGE) protein shown in AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of canine allergies

SQ Sequence 20 AA;

Query Match 75.0%; Score 102; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKA 19

Db 2 CRVTHPLPKDIVRSIAKA 20

```

RESULT 2
AAV50894
ID   AAY50894 standard; peptide; 17 AA.
XX
XX   AC   AAY50894;
XX
XX   DT   24-FEB-2000 (first entry)
XX
XX   DE   Antibody 15A.2 canine IgE binding epitope 1.
XX
XX   KW   Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX   KW   epitope; prophylaxis; treatment; mimotope.
XX
XX   OS   Synthetic.
XX
XX   PN   EP957111-A2.
XX
XX   PD   17-NOV-1999.
XX
XX   PF   09-APR-1999; 99EP-00107035.
XX
XX   PR   09-APR-1998; 98US-00058331.
XX   PR   30-MAR-1999; 99US-00281760.
XX
XX   PA   (INDEX-) IDEXX LAB INC.
XX
XX   PI   Lawton R, Mermer B, Francoeur G;
XX
XX   DR   WPI; 2000-040833/04.
XX
XX   PT   Binding proteins used for treatment or prophylaxis of canine allergy.
XX
XX   PS   Disclosure; Fig 7; 30pp; English.
XX
XX   CC   This invention describes a novel binding protein which specifically binds
XX   CC   to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX   CC   when the IgE is bound to mast cells. The peptide products of the
XX   CC   invention have anti-allergic activity. The antibodies bind to defined
XX   CC   epitopes on free or B-cell bound IgE molecules which have an important
XX   CC   role in allergic reaction. The specific binding proteins are used to
XX   CC   produce a pharmaceutical composition, preferably with a diluent, which
XX   CC   can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX   CC   Y50900 represent peptide mimotopes used in the method of the invention
XX
XX   SQ   Sequence 17 AA;
XX
XX   PI   Lawton R, Mermer B, Francoeur G;
XX
XX   DR   WPI; 2000-040833/04.
XX
XX   PT   Binding proteins used for treatment or prophylaxis of canine allergy.
XX
XX   PS   Disclosure; Fig 7; 30pp; English.
XX
XX   CC   This invention describes a novel binding protein which specifically binds
XX   CC   to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX   CC   when the IgE is bound to mast cells. The peptide products of the
XX   CC   invention have anti-allergic activity. The antibodies bind to defined
XX   CC   epitopes on free or B-cell bound IgE molecules which have an important
XX   CC   role in allergic reaction. The specific binding proteins are used to
XX   CC   produce a pharmaceutical composition, preferably with a diluent, which
XX   CC   can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX   CC   Y50900 represent peptide mimotopes used in the method of the invention
XX
XX   SQ   Sequence 17 AA;

Query Match      65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 CRVTHPLPKDIVRSI 16
Db    1 CRVTHPLPKDIVRSI 17

RESULT 3
AAV50893
ID   AAY50893 standard; peptide; 17 AA.
XX
XX   AC   AAY50893;
XX
XX   DT   24-FEB-2000 (first entry)
XX
XX   DE   Antibody 15A.2 binding peptide 10 from PhDc7c phage display library.
XX
XX   KW   Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX   KW   epitope; prophylaxis; treatment; mimotope.
XX
XX   OS   Synthetic.
XX
XX   PN   EP957111-A2.
XX
XX   PD   17-NOV-1999.
XX
XX   PF   09-APR-1999; 99EP-00107035.
XX
XX   PR   09-APR-1998; 98US-00058331.
XX   PR   30-MAR-1999; 99US-00281760.
XX
XX   PA   (INDEX-) IDEXX LAB INC.
XX
XX   PI   Lawton R, Mermer B, Francoeur G;
XX
XX   DR   WPI; 2000-040833/04.
XX
XX   PT   Binding proteins used for treatment or prophylaxis of canine allergy.
XX
XX   PS   Disclosure; Fig 7; 30pp; English.
XX
XX   CC   This invention describes a novel binding protein which specifically binds
XX   CC   to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX   CC   when the IgE is bound to mast cells. The peptide products of the
XX   CC   invention have anti-allergic activity. The antibodies bind to defined
XX   CC   epitopes on free or B-cell bound IgE molecules which have an important
XX   CC   role in allergic reaction. The specific binding proteins are used to
XX   CC   produce a pharmaceutical composition, preferably with a diluent, which
XX   CC   can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX   CC   Y50900 represent peptide mimotopes used in the method of the invention
XX
XX   SQ   Sequence 17 AA;

Query Match      65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 CRVTHPLPKDIVRSI 16
Db    1 CRVTHPLPKDIVRSI 17

RESULT 4
AAV79999
ID   AAY79999 standard; peptide; 25 AA.
XX
XX   AC   AAY79999;
XX
XX   DT   15-MAY-2000 (first entry)
XX
XX   DE   Optimised IgE-CH3 domain antigen peptide for dog IgE.
XX
XX   KW   Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX   KW   immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX   KW   antibody; allergy; allergic disease; immunisation; anti-allergic;
XX   KW   anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX   OS   Canis sp.
XX   OS   Synthetic.
XX
XX   PN   WO9967293-A1.
XX
XX   PD   29-DEC-1999.
XX
XX   PF   21-JUN-1999; 99WO-US013959.
XX
XX   PR   20-JUN-1998; 98US-00100287.
XX
XX   PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
XX   PI   Wang CY, Walfield AM;
XX   PI   WPI; 2000-160578/14.
XX
XX   PT   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX   PT   for immunization against allergy.
XX

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PD   17-NOV-1999.
XX
XX   PF   09-APR-1999; 99EP-00107035.
XX
XX   PR   09-APR-1998; 98US-00058331.
XX   PR   30-MAR-1999; 99US-00281760.
XX
XX   PA   (INDEX-) IDEXX LAB INC.
XX
XX   PI   Lawton R, Mermer B, Francoeur G;
XX
XX   DR   WPI; 2000-040833/04.
XX
XX   PT   Binding proteins used for treatment or prophylaxis of canine allergy.
XX
XX   PS   Disclosure; Fig 6; 30pp; English.
XX
XX   CC   This invention describes a novel binding protein which specifically binds
XX   CC   to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX   CC   when the IgE is bound to mast cells. The peptide products of the
XX   CC   invention have anti-allergic activity. The antibodies bind to defined
XX   CC   epitopes on free or B-cell bound IgE molecules which have an important
XX   CC   role in allergic reaction. The specific binding proteins are used to
XX   CC   produce a pharmaceutical composition, preferably with a diluent, which
XX   CC   can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX   CC   Y50900 represent peptide mimotopes used in the method of the invention
XX
XX   SQ   Sequence 17 AA;

Query Match      65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 CRVTHPLPKDIVRSI 16
Db    1 CRVTHPLPKDIVRSI 17

RESULT 4
AAV79999
ID   AAY79999 standard; peptide; 25 AA.
XX
XX   AC   AAY79999;
XX
XX   DT   15-MAY-2000 (first entry)
XX
XX   DE   Optimised IgE-CH3 domain antigen peptide for dog IgE.
XX
XX   KW   Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX   KW   immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX   KW   antibody; allergy; allergic disease; immunisation; anti-allergic;
XX   KW   anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX   OS   Canis sp.
XX   OS   Synthetic.
XX
XX   PN   WO9967293-A1.
XX
XX   PD   29-DEC-1999.
XX
XX   PF   21-JUN-1999; 99WO-US013959.
XX
XX   PR   20-JUN-1998; 98US-00100287.
XX
XX   PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
XX   PI   Wang CY, Walfield AM;
XX   PI   WPI; 2000-160578/14.
XX
XX   PT   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX   PT   for immunization against allergy.
XX

```

PS Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY7994 to AAY8084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX SQ Sequence 25 AA;

Query Match 65.4%; Score 89; DB 3; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
 DB 8 RVTHPHLPKDIVRSIAK 24
 |||||

RESULT 5

AAW24103
 ID AAW24103 standard; peptide; 20 AA.

XX AC AAW24103;

XX 21-NOV-1997 (first entry)

XX Canine immunoglobulin E peptide 6.

XX Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.

XX Canis familiaris.

XX JP09169795-A.

XX 30-JUN-1997.

XX 22-DEC-1995; 95JP-00334381.

XX 22-DEC-1995; 95JP-00334381.

XX (HITB) HITACHI CHEM CO LTD.

XX WPI; 1997-389423/36.

XX N-PSDB; AAT85652.

XX Canine immunoglobulin E peptide fragment and related DNA - useful for the
 PT preparation of anti-canine immunoglobulin E antibody.

XX Claim 2; Page 9; 12pp; Japanese.

XX AAW24098-106 are peptide fragments containing at least 5 continuous amino
 CC acids of the partial canine immunoglobulin E (IgE) protein shown in
 CC AAW24097. The peptides are used for the preparation of anti-canine IgE
 CC antibody. The anti-canine IgE antibody can be used for the diagnosis of
 CC canine allergies

XX SQ Sequence 20 AA;

Query Match 58.1%; Score 79; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KDIVRSIAKAPGKRAP 25
 DB 1 KDIVRSIAKAPGKRAP 16
 |||||

RESULT 6

AAV50896
 ID AAV50896 standard; peptide; 17 AA.

XX AC AAV50896;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 green monkey IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
 XX epitope; prophylaxis; treatment; mimotope.

XX OS Synthetic.

XX PN EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-00107035.

XX 09-APR-1998; 98US-00058331.

XX 30-MAR-1999; 99US-00281760.

XX (IDEX-) IDEXX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy.

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically binds
 CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE
 CC when the IgE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IgE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-
 CC Y50900 represent peptide mimotopes used in the method of the invention

XX SQ Sequence 17 AA;

Query Match 52.9%; Score 72; DB 3; Length 17;
 Best Local Similarity 80.0%; Pred. No. 0.00047;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRS 15
 DB 2 CRVTHPHLPALVRS 16
 |||||

RESULT 7

AAV50895
 ID AAV50895 standard; peptide; 17 AA.

XX AC AAV50895;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 human IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KW epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-00107035.
 XX
 PR 09-APR-1998; 98US-00058331.
 PR 30-MAR-1999; 99US-00281760.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX
 PT Binding proteins used for treatment or prophylaxis of canine allergy.
 XX
 PS Disclosure; Fig 7; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy. AAY50876-Y50900 represent peptide mimotopes used in the method of the invention
 XX
 CC Sequence 17 AA;
 SQ
 Query Match 50.7%; Score 69; DB 3; Length 17;
 Best Local Similarity 73.3%; Pred. No. 0.0014;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRVTHPLPKDIVRS 15
 DB |||||:::|
 2 CRVTHPLFRLMRS 16
 RESULT 8
 AAY80000
 ID AAY80000 standard; peptide; 25 AA.
 XX
 AC AAY80000;
 XX
 DT 15-MAY-2000 (first entry)
 XX
 DE Optimised IgE-CH3 domain antigen peptide for rat IgE.
 XX
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 PN WO9967293-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US013959.
 XX
 PR 20-JUN-1998; 98US-00100287.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.
 DR
 XX
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
 XX
 PS Claim 1; Page 99; 155pp; English.
 XX
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
 XX
 CC Sequence 25 AA;
 SQ
 Query Match 50.0%; Score 68; DB 3; Length 25;
 Best Local Similarity 76.5%; Pred. No. 0.003;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 RVTHPLPKDIVRSIAK 18
 DB |||||:::|
 8 RVDRHPFKPIVRSITK 24
 RESULT 9
 AAY50898
 ID AAY50898 standard; peptide; 17 AA.
 XX
 AC AAY50898;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 swine IgE binding epitope 1.
 XX
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 XX
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-00107035.
 XX
 PR 09-APR-1998; 98US-00058331.
 PR 30-MAR-1999; 99US-00281760.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Lawton R, Mermer B, Francoeur G;
 XX
 DR WPI; 2000-040833/04.
 XX
 PT Binding proteins used for treatment or prophylaxis of canine allergy.
 XX
 PS Disclosure; Fig 7; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE

CC when the Ige is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound Ige molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AAY50876-
CC Y50900 represent peptide mimotopes used in the method of the invention
XX SQ Sequence 17 AA;

Query Match 47.8%; Score 65; DB 3; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0057;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
DB 2 CNVTHPLPKDIVRSI 17

RESULT 10
AAY68602
ID AAY68602 standard; peptide; 25 AA.
XX
AC AAY68602;
XX
DT 05-MAY-2000 (first entry)
XX
DE Peptide sequence of the invention.
XX
KW Helper T cell epitope; peptide immunogen; LHRH;
KW luteinizing hormone-releasing hormone; spermatogenesis; ovulation;
KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.
XX
OS Unidentified.
XX
PN WO9966952-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013960.
XX
PR 20-JUN-1998; 98US-00100414.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160562/14.
XX
PT New peptide immunogen containing luteinizing hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer.
XX
PS Disclosure; Page 92; 102pp; English.
XX
CC The specification describes peptide immunogens comprising a synthetic
CC helper T cell (Th) epitope and a target antigen, luteinising hormone-
CC releasing hormone (LHRH). The peptide immunogens cause induction of a
CC specific immune response to LHRH which is involved in regulation of
CC spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC sex hormones. Provision of a promiscuous T helper epitope (which is
CC functional in genetically diverse subjects) provides optimum
CC immunogenicity to the B cell epitopes of the target antigen and thus high
CC antibody titres against the target antigen. The peptide immunogens of the
CC invention are used to vaccinate against mammalian LHRH, for use as
CC (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC of prostate or breast, also endometriosis); to prevent boar taint (and
CC improve meat quality) and for immunocastration. The present sequence
CC appears in the specification
XX SQ Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.013;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
DB 8 RVTHPLPALMRSTTK 24

RESULT 11
AAY91212
ID AAY91212 standard; peptide; 25 AA.
XX
AC AAY91212;
XX
DT 22-MAY-2000 (first entry)
XX
DE Modified human Ige CH3 domain, SEQ ID NO:92.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; Ige; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CPTp;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Example 6; Page 40; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CPTp) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone-
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)

CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin, and a Th
 CC epitope. Somatostatin immunogens may be used to promote growth in
 CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
 CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified
 CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
 CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
 CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
 CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
 CC AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are
 CC immunogens comprising a CERP peptide and a Th epitope which may be used
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
 CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
 CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
 CC both of which may optionally be used in the antigenic peptides of the
 CC invention

XX Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.013;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
 |||||:::|
 Db 8 RVTHPHLPALMRSTTK 24

RESULT 12

ID AAY79998 standard; peptide; 25 AA.

XX AC AAY79998;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.
 OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.

XX Claim 1; Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IgE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;
 Best Local Similarity 64.7%; Pred. No. 0.013;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18
 |||||:::|
 Db 8 RVTHPHLPALMRSTTK 24

RESULT 13

ID AAY80077 standard; peptide; 25 AA.

XX AC AAY80077;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for horse IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Equus caballus.
 OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.

XX Claim 1; Page 146; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IgE, and so

preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79594 to AAY80084 represent amino acid sequences used in the exemplification of the present invention

Sequence 25 AA;

Query Match 46.3%; Score 63; DB 3; Length 25;
Best Local Similarity 68.8%; Pred. NO. 0.018;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY	3	VTTHPLEKDIERSIAK	18
		: :	
		: :	
D _b	9	VSHPDLPREVVSIAK	24

RESULT 14
 RAY50897
 ID RAY50897 standard; peptide; 17 AA.
 XX
 AC
 XX RAY50897;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 15A.2 feline IGE binding epitope 1.

Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
KW
epitope; prophylaxis; treatment; mimotope.
KW

OS Synthetic.

PN EP957111-A2.

17-NOV-1999.

09-APR-1999: 99EP-00107035.

XX 09-APR-1998: 9AUS-00058331 PR

PR 30-MAR-1999; 99US-00281760.

PA (INDEX-) IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

DR WPI; 2000-040833/04.

PT Binding proteins used for treatment or prophylaxis of canine allergy.

PS Disclosure: Fig 7: 30pp: English.

This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy. **RAY50876-1** y50900 represent peptide mimotopes used in the method of the invention

Sequence 17 AA;

Query Match	44.9%;	Score 61;	DB 3;	Length 17;
Best Local Similarity	75.0%;	Pred. No. 0.024;		

Matches	12;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0
QY	1	CRVTHPHLPKDI	VSRI	16					
		: : :	: : :						
Db	2	CKVTHPDLP	LVRSI	17					
RESULT 15									
AAO18028									
ID	AAO18028 standard; peptide; 14 AA.								
XX									
AC	AAO18028;								
XX									
DT	30-AUG-2002 (first entry)								
XX									
DE	Human immunoglobulin E epitope SEQ ID NO: 20.								
XX									
KW	Allergy; immunoglobulin E; iGE; vaccine; immunogen; epitope; human;								
KW	non-anaphylactogenic; anti-allergic.								

XX
SO
Homo sapiens.

XX
PN
WO200234288-A2.

XX
PD 02-MAY-2002XX
PF
24-OCT-2001 - 2001WO-EP012392

XX
DP 27-00T-2000. 2000GB-00026334

XX
DA /CMTV\ CMTTUT TNE DEECUM ET

XX
XX

XX

XX

PT or preventing allergies, for typing circulating anti-IgE, or for
PT diagnosing atopy.

PS Claim 1; Page 5; 28pp; English.

The present invention provides peptide epitopes derived from human immunoglobulin E (IgE), which are non-anaphylactogenic and can be used as immunogens to diagnose and treat allergies. The present sequence is an epitope of the invention

Sequence 14 AA;

Query Match	44.1%	Score 60;	DB 5;
Best Local Similarity	69.2%;	Pred. No. 0.027;	
Matches 9;	Conservative 3;	Mismatches 1;	Indels 0;
Matches 0;	Gaps 0;		

QY 1 CRVTHPHLPKDIV 13

Db 1 CRVTHPLPALM 13

Search completed: March 18, 2004, 14:00:20
Job time : 54 secs